



NTNU – Trondheim
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Department of Biology

Examination paper for BI3019

Systems Biology: Resources, standards and tools

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Exam Questions BI3019 – 13 December 2014 - Systems Biology

Your answers should typically be at least ½ page of written text.

One question can be skipped (optional)

1. High throughput technologies are often ‘noisy’, meaning that some of the data that they produce does not concern biological information but random signals: noise. Describe two examples of technologies and the type of noise they produce, and suggest analysis approaches that you could use to become more confident about the data. In your answer you may mention reliability, confidence, sensitivity and false positives/false negatives.
2. Describe what is meant with the name ‘transcriptome’; describe how transcriptome information can be generated (mention technologies as well as experimental designs) and explain how this type of information can be integrated with other ‘omics’ data.
3. Describe the Reactome database, explain how it is built, discuss data formats and exchange mechanisms and describe at least two analysis methods that Reactome supports.
4. Describe the different steps in a systems biology approach to study a biological process, and discuss how, following these steps, you can use a computer to develop a better understanding of the biological process.
5. Describe three different types of networks composed of nodes and edges, focusing on how well network nodes are connected. Describe at least two network metrics that you can use to characterise these different networks and demonstrate that they are different. Relate your observations to biological networks.
6. Explain what the MIAME checklist stands for, why it is important for data integration, and how it has helped to create valuable databases.
7. Ontologies provide an important resource for analysing experimental data. Describe at least 3 different ways in which a computer can use ontologies in order to provide insight in experimental results.

8. You have performed a microarray analysis of the transcriptome of *Arabidopsis thaliana*, grown under a variety of stress types and normal conditions. Explain how you would analyse the data to provide insight about biological processes that respond to stress in *Arabidopsis*.
9. Compare Boolean modelling with Ordinary Differential Equation modelling, discuss the amount and type of data that you need for these different approaches, and potential quality of the output.
10. Cytoscape and CellDesigner are two tools that can be used for analyzing experimental results. Describe the similarities and differences of these two tools, and provide at least two examples of analysis that you can do with these tools.
11. Name two different text mining tools; describe how they work, what text mining principles they use, and how they can be used to identify new candidates for a biological network that you are studying.
12. You join a research group who study the effects of the hormone gastrin on growth of a human cell line using a traditional approach focusing on single genes and proteins. Write down three arguments that you would use to persuade your colleagues to use a systems approach.
13. Provide brief descriptions of the Biomodels knowledgebase, the STRING database base and the PANTHER database. You may consider for instance the type of data/knowledge in these resources, the functionality provided and the integration of information in these databases with other resources.